UDESC

Characterization of rice genotypes used in Brazil regarding salinity tolerance at the seedling stage

Caracterização de genótipos de arroz utilizados no Brasil quanto à tolerância à salinidade no estádio de plântula

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ABSTRACT

Rice production (*Oryza sativa* L.) is among the most economically important activities in the world. However, soil and salinity coming from irrigation water reduce rice yield. Therefore, the identification and/or development of salt-tolerant rice genotypes is a strategy to minimize this problem. The development of new genotypes depends on the presence of genetic diversity, and understanding the heritability of a desired trait can help in the selection process. Thus, this study aimed to identify superior genotypes, analyze the genetic diversity and estimate the heritability for salinity tolerance at the seedling stage in rice genotypes used in Brazil. For this, seedlings of 69 genotypes were kept in hydroponic solution with 40 mM NaCl (4 dSm^{-1}) for seven days. Shoot length, root length, shoot dry weight, and root dry weight) were evaluated and the results were converted into relative performance. Tolerant and moderately salt-tolerant genotypes were identified at the seedling stage, which can be used in breeding programs and can be cultivated in high salinity areas. Principal component analysis showed the presence of genetic diversity for salinity response. Finally, it was shown that most of the observed variation is of genetic origin, which can make the breeding process less difficult.

KEYWORDS: abiotic stress; agronomic traits; genetic diversity; heritability; *Oryza sativa* L.

RESUMO

O arroz (*Oryza sativa* L.) é uma espécie com grande importância econômica no mundo. A salinidade do solo ou da água reduz a produtividade da cultura. Por isso, a identificação e/ou desenvolvimento de genótipos de arroz com tolerância à salinidade é uma estratégia para minimizar esse problema. O desenvolvimento de novos genótipos depende da presença de variabilidade genética, e o conhecimento da herdabilidade da característica de interesse pode auxiliar no processo de seleção. Dessa forma, esse estudo teve como objetivo identificar genótipos superiores, analisar a variabilidade genética e estimar a herdabilidade para tolerância a salinidade no estádio de plântula em genótipos de arroz utilizados no Brasil. Para isso, plântulas de 69 genótipos foram mantidas em solução hidropônica acrescida de 40mM de NaCl (4 dSm^{-1}) durante sete dias. Foram avaliados comprimento de parte aérea, comprimento de raiz, peso seco de parte aérea, e peso seco de raiz e os resultados foram convertidos em desempenho relativo. Foram identificados genótipos tolerantes e moderadamente tolerantes à salinidade no estádio de plântula, os quais podem ser utilizados em programas de melhoramento e cultivados em áreas com ocorrência desse estresse. A análise de componentes principais mostrou a presença de variabilidade genética para resposta à salinidade. Finalmente, foi demonstrado que a maior parte da variação observada nos caracteres é de origem genética, o que pode tornar o processo de melhoramento menos difícil.

PALAVRAS-CHAVE: estresse abiótico; caracteres agronômicos; variabilidade genética; herdabilidade; *Oryza sativa* L.

INTRODUCTION

Rice (*Oryza sativa* L.) is a source of calories for more than half of the world's population. Out of Asian countries, Brazil is the main producer and consumer of rice. Most rice production occurs in Southern Brazil,

in the Rio Grande do Sul (RS) state (OLIVEIRA et al. 2021). In the RS, rice is cultivated under flood irrigation. The fields located on the coastal plain, irrigation water comes mainly from the Lagoon "Laguna dos Patos", which is connected to the Atlantic Ocean. The reproductive stage, when the crop demands a lot of water, coincides with a low rain period, reducing the level of the Lagoon, and culminating with the entry of water from the Ocean, causing water salinization. Water with high salt level can result in direct damage to the crop, and in addition, cause soil salinity, which will affect future harvest seasons. Electrical conductivity (EC) in irrigation channels using water from Laguna dos Patos has been shown to range from 0.5 dS m^{-1} to 6.0 dS m^{-1} and sometimes beyond these extremes (DENARDIN et al. 2020).

A soil is considered saline when it has an EC above 4 dS m^{-1}; however, rice is a salt-sensitive crop with a threshold of 3 dS m^{-1} (HOANG et al. 2016). Rice yield losses increase as EC increases (HOANG et al. 2016). Rice plants respond to salt stress differently according to the developmental stage, being relatively tolerant during germination, tillering and maturation and very sensitive in the seedling and reproductive stages (SINGH et al. 2021a). In the RS, salt stress at seedling stage can be due to irrigation with salt water or by the occurrence of saline soils as a result salt water used in previous harvest seasons. Salinity stress at the seedling stage can affect crop yield because it interferes with the performance of some yield components (KAKAR et al. 2019). Thus, salt-tolerance at seedling stage should be considered during the genetic improvement of rice varieties.

Crossing-over and mutations are responsible for genetic diversity. The presence of genetic diversity is required for a successful breeding program. Thus, the development of superior genotypes depends on the nature and magnitude of the genetic diversity available in the parents used in the crosses, favoring the potential of genetic recombination (SINGH et al. 2021b). It has been suggested that rice has wide genetic diversity for salt tolerance, which can be accessed in different germplasm banks for use in breeding programs. Due to the large number of accessions with moderate salt-tolerance, some authors suggest that the species can be classified as moderately tolerant (SINGH et al. 2021a).

Another important factor for the success of breeding programs is the estimation of the trait heritability, a precision measure that allows determining the selection response. Narrow-sense heritability (h^2) is the proportion of phenotypic variation between individuals attributed to heritable genetic effects (additive effects), while broad-sense heritability (H^2) is the proportion of phenotypic variation attributed to the combination of the additive, dominance and epistatics effects (PIEPHO & MÖHRING 2007).

Some studies aimed at characterizing the genetic diversity for salinity tolerance at the seedling stage in rice (KANAWAPEE et al. 2011, ALI et al. 2014, DE LEON et al. 2015, EMON et al. 2015, KAKAR et al. 2019) as well as estimate the heritability for this trait (GREGORIO & SENADHIRA 1993, MOHAMMADI et al. 2014, PURAM et al. 2017). However, to our knowledge, studies of genetic diversity and heritability for salinity tolerance at seedling stage in rice genotypes used in Brazil have not yet been performed. In this sense, the objective of this work was to identify superior genotypes, analyze the genetic diversity and estimate the heritability for salinity tolerance in rice seedlings, in a collection of genotypes used in Brazil.

MATERIALS AND METHODS

This study analyzed a collection of 69 rice accessions (commercial cultivars and accessions available in germplasm banks) used in Brazil. Initially, the seeds were disinfected with alcohol 70% (v/v) for one minute, washed with distilled water, and later were submerged in a solution of sodium hypochlorite (NaClO) 4% (v/v) for five minutes and finally, they were washed twice with distilled water. The seeds were placed in a Gerbox-type container for germination, using Germitest-type paper as substrate. The paper was soaked with distilled water in an amount equivalent to 2.5 times its weight. The boxes were placed in a BOD germination chamber at 25 °C, with a photoperiod of 16 hours, for seven days.

After this period, seedlings with a uniform root length (about 5 mm) were transplanted into pots with nylon screens, fitted in 750 mL containing rice standard nutrient solution, prepared according to the modified protocol by YOSHIDA (1981). In the control, standard solution was used and in salt stress the nutrient solution was added of 40 mM of NaCl or EC of ~4.0 dS m^{-1}. After preparing the solution, the pH was adjusted to 4.5 (FAGERIA et al. 1990, GREGORIO et al. 1997) using HCl acid or NaOH base and later fixed with the chemical reagent MES [monohydrate: 2 - (N-Morpholino) ethanesulfonic acid hydrate]. The pots were placed in a hydroponic tank with artificial light, with a photoperiod of 16/8 hours (light/dark) and controlled temperature of 25 ± 1 °C, for seven days. The experimental design was randomized blocks, with five biological replicates consisting of 10 seedlings each.

Shoot length (SL), root length (RL), shoot dry weight (SDW), and root dry weight (RDW) traits were evaluated in five seedlings of each replicate under control and salinity stress (40 mM NaCl) conditions.

Length analyzes were performed with the aid of a graduated ruler and the results were expressed in centimeters. Each seedling was cut at the junction between root and shoot for the dry mass weight, and the tissues were dried in an air forced oven at 70 °C, until reaching constant weight, then were weighed using a precision scale (Marte®). Considering that the studied genotypes present intrinsic developmental characteristics, results were transformed in relative performance (RP), dividing the value in the stress condition by the value obtained in the control condition (TEJEDA et al. 2020).

The results were subjected to the normality test, followed by the analysis of variance (ANOVA). Afterward, the Scott-Knott means test was performed (p<0.05). To verify the presence of genetic diversity regarding the salinity response, the values were subjected to principal component analysis (PCA). Finally, the broad sense heritability estimate (H^2) was calculated. The analyzes were performed using the R Software (R CORE TEAM 2020).

RESULTS

The genotype significantly influenced the shoot, root and dry mass deposition response in rice seedlings subjected to salinity (Table 1). In some genotypes, salinity stress affects the shoot and root in a similar way, while in others, the tissues respond differently to salinity (Table 2).

Table 1. Summary of variance and heritability analysis for 69 rice genotypes in the seedling stage grown under salinity.

Source		Mean Square			
	df[±]	SL	RL	SDW	RDW
Block	4	0.1462	0.0195	0.0273	0.0813
Genotype	68	0.0481[*]	0.0733[*]	0.0627[*]	0.0995[*]
Error	195	0.0197	0.018	0.0130	0.0269
cv (%)		19.88	14.96	14.26	20.63
H² (%)		0.59	0.75	0.79	0.72

[*]Significant at p≤0.0001 by the F test. [±]df: degrees of freedom; cv: coefficient of variation; H^2: broad sense heritability; SL: shoot length; RL: root length; SDW: shoot dry weight and RDW: root dry weight.

For shoot length (SL), relative performance (RP) the genotypes were distributed into three groups according to salinity response, RP 1.13 – 1.10 (2 genotypes), RP 0.9 – 0.72 (30 genotypes) and RP 0.71 – 0.43 (37 genotypes). For root length (RL), the genotypes were also divided into three groups, RP 1.29 – 1.12 (8 genotypes), RP 1.09 – 0.98 (11 genotypes) and RP 0.94 – 0.64 (50 genotypes). Considering the shoot dry mass (SDW) four groups were formed, RP 1.42 (1 genotype), RP 1.09 – 0.80 (34 genotypes), RP 0.78 – 0.58 (31 genotypes) and RP 0.47 – 0.33 (3 genotypes). Finally, based on root dry mass (RDW) the genotypes were distributed into three groups, RP 1.20 – 0.98 (9 genotypes), RP 0.94 – 0.78 (31 genotypes) and RP 0.76 – 0.31 (29 genotypes) (Table 2).

Based on the mean relative performance of the four traits in response to salinity at the seedling stage, the genotypes were clustered into four categories: tolerant = RP ≥ 0.9 (10 genotypes); moderately tolerant = 0.8 ≤ RP < 0.9 (27 genotypes); moderately sensitive = 0.7 ≤ RP < 0.8 (20 genotypes) and sensitive = RP < 0.7 (12 genotypes) (Table 2).

Table 2. Means grouping of relative performance (RP) of traits evaluated in 69 rice genotypes in seedling stage grown under salinity stress.

	SL		RL		SDW		RDW		Mean	Group
TOX-514-16-101-1	0.51	c	0.66	c	0.45	d	0.31	c	0.48	S
SC-460	0.43	c	0.75	c	0.47	d	0.59	c	0.56	S
BRS-Fronteira	0.56	c	0.76	c	0.69	c	0.60	c	0.65	S
Nowrin-Mochi	0.68	c	0.64	c	0.69	c	0.64	c	0.66	S
SCS-121-CL	0.58	c	0.74	c	0.67	c	0.66	c	0.66	S
SCS-117-CL	0.68	c	0.74	c	0.72	c	0.54	c	0.67	S
SCS-BRS-Tio-Taka	0.68	c	0.82	c	0.67	c	0.52	c	0.67	S
Tomoe-Mochi	0.58	c	0.91	c	0.33	d	0.89	b	0.68	S
IRGA-427	0.62	c	0.91	c	0.77	c	0.42	c	0.68	S
BR-IRGA-410	0.48	c	0.81	c	0.82	b	0.64	c	0.69	S
Zebu	0.68	c	0.84	c	0.67	c	0.56	c	0.69	S
Empasc-103	0.63	c	0.88	c	0.63	c	0.63	c	0.69	S
To be continued...										

Continuation Table 2...

IRAT-124	0.63	c	0.74	c	0.67	c	0.75	c	0.70	MS
Qualimax	0.59	c	0.83	c	0.66	c	0.75	c	0.71	MS
IRGA-419	0.74	b	0.67	c	0.73	c	0.71	c	0.71	MS
SCS-112	0.70	c	0.87	c	0.70	c	0.61	c	0.72	MS
BRS-A-701-CL	0.58	c	0.74	c	0.82	b	0.75	c	0.72	MS
M1313	0.71	c	0.70	c	0.69	c	0.81	b	0.73	MS
BRS-7-Taim	0.69	c	0.66	c	0.85	b	0.74	c	0.74	MS
BRS-358	0.79	b	0.81	c	0.76	c	0.62	c	0.75	MS
SCS-114-Andosan	0.72	b	0.79	c	0.68	c	0.80	b	0.75	MS
SCS-115-CL	0.67	c	0.71	c	0.78	c	0.83	b	0.75	MS
SCS-118-Maiques	0.70	c	0.99	b	0.78	c	0.55	c	0.76	MS
SCS-116-Satoru	0.71	c	0.91	c	0.78	c	0.62	c	0.76	MS
Austral	0.80	b	0.99	b	0.70	c	0.55	c	0.76	MS
EPAGRI-107	0.67	c	0.79	c	0.75	c	0.84	b	0.76	MS
BRS-6-Chuí	0.68	c	1.02	b	0.78	c	0.63	c	0.78	MS
BR-IRGA-409	0.73	b	0.80	c	0.83	b	0.76	c	0.78	MS
EPAGRI-106	0.66	c	0.80	c	0.80	b	0.90	b	0.79	MS
M1410	0.73	b	0.83	c	0.83	b	0.78	b	0.79	MS
Guri-INTA-CL	0.70	c	0.81	c	0.83	b	0.83	b	0.79	MS
BRS-Pampeira	0.55	c	0.93	c	0.75	c	0.94	b	0.79	MS
IRGA-428	0.77	b	0.87	c	0.76	c	0.80	b	0.80	MT
IRGA-429	0.68	c	0.78	c	0.83	b	0.92	b	0.80	MT
SCS-120-Onix	0.73	b	1.05	b	0.76	c	0.68	c	0.81	MT
EPAGRI-109	0.75	b	0.87	c	0.78	c	0.82	b	0.81	MT
Amarelo-B	0.67	c	1.09	b	0.67	c	0.82	b	0.81	MT
Carolina	1.13	a	0.67	c	0.67	c	0.79	b	0.82	MT
BRS-Pampa	0.66	c	1.12	a	0.78	c	0.71	c	0.82	MT
Arborio	0.78	b	0.84	c	0.83	b	0.83	b	0.82	MT
SCS-BRS-111	0.85	b	0.88	c	0.88	b	0.70	c	0.83	MT
Tetep	0.60	c	1.29	a	0.58	c	0.84	b	0.83	MT
BR-IRGA-412	0.89	b	1.00	b	0.93	b	0.49	c	0.83	MT
IRGA-417	0.86	b	0.88	c	0.80	b	0.79	b	0.83	MT
EPAGRI-108	0.72	b	0.98	b	0.85	b	0.80	b	0.84	MT
SCS-119-Rubi	0.73	b	0.80	c	0.95	b	0.86	b	0.84	MT
Carnaroli	0.61	c	0.91	c	0.88	b	0.98	a	0.85	MT
MNA-PB-0405	0.74	b	0.90	c	1.01	b	0.73	c	0.85	MT
IRAT-162	0.76	b	0.85	c	0.86	b	0.92	b	0.85	MT
Empasc-102	0.80	b	0.94	c	0.83	b	0.82	b	0.85	MT
BRS-Querência	0.74	b	1.06	b	0.67	c	0.92	b	0.85	MT
Cacho-Grande	0.87	b	0.87	c	0.84	b	0.82	b	0.85	MT
IRGA-420	0.50	c	1.00	b	0.84	b	1.08	a	0.86	MT
BRS-Sinuelo-CL	0.60	c	0.88	c	0.80	b	1.16	a	0.86	MT
BRS-AG	0.77	b	1.01	b	0.91	b	0.79	b	0.87	MT
IRGA-418	0.62	c	1.18	a	0.90	b	0.79	b	0.87	MT
BRS-IRGA-414	0.69	c	0.80	c	0.89	b	1.13	a	0.88	MT
IRGA-424-RI	0.90	b	0.90	c	0.90	b	0.82	b	0.88	MT
SC-173	0.43	c	0.75	c	1.42	a	0.94	b	0.89	MT
M1150	0.78	b	1.17	a	0.82	b	0.81	b	0.90	T
Lemont	0.75	b	0.93	c	0.89	b	1.07	a	0.91	T
Empasc-101	0.74	b	1.29	a	0.77	c	0.85	b	0.91	T
BRS-Bojuru	0.77	b	1.16	a	0.90	b	0.83	b	0.92	T
Meio-Chumbinho	0.67	c	0.94	c	1.00	b	1.13	a	0.94	T
Empasc-105	0.77	b	0.93	c	0.87	b	1.20	a	0.94	T
Empasc-104	0.75	b	1.02	b	0.99	b	1.06	a	0.96	T
IAS-12-9-Formosa	0.79	b	1.26	a	1.09	b	0.73	c	0.97	T
Empasc-100	0.88	b	0.85	c	0.96	b	1.20	a	0.97	T
Rexoro	1.10	a	1.18	a	0.91	b	0.93	b	1.03	T

SL: shoot length; RL: root length; SDW: shoot dry weight; RDW: root dry weight; S: sensitive; MS: moderately sensitive; MT: moderately tolerant and T: tolerant. Means followed by the same lowercase letter in the column do not differ by the Scott-Knott test ($p \leq 0.05$).

Principal component analysis allowed the separation of rice accessions according to salinity response, with tolerant or moderately tolerant genotypes located on the right of the graph and moderately sensitive and sensitive genotypes allocated on the left (Figure 1).
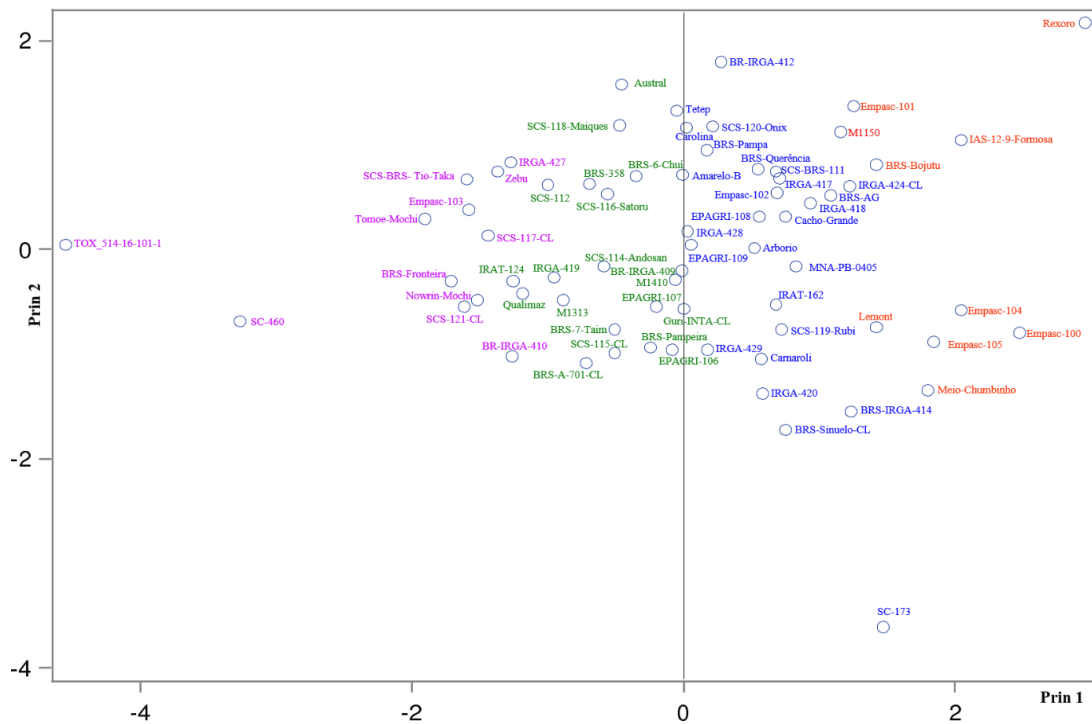
Figure 1. Principal component analysis based on the relative performance of the traits shoot length (SL), root length (RL), shoot dry weight (SDW), and root dry weight (RDW) in 69 rice genotypes in the seedling stage grown under salinity stress. The principal component 1 explains 42% of the variation and the principal component 2 explains 24%. Genotypes in red: tolerant; genotypes in blue: moderately tolerant; genotypes in purple: moderately sensitive and genotypes in green: sensitive.

Considering the salinity response of rice seedlings, the heritability in the broad sense (H^2) was 0.59 for SL, 0.75 for RL, 0.79 for SDW and 0.72 for RDW (Table 1).

DISCUSSION

Rice has a variable salinity response according to the development stage, with sensitivity in the seedling and reproductive stages. Salinity tolerance at the seedling stage contributes to the maintenance of crop yield since, at this stage, stress can affect yield components, such as the number of tillers per plant, shoot biomass, flowering time, and harvest index (KAKAR et al. 2019). Therefore, the characterization and/or screening of genotypes for salinity tolerance at the seedling stage is essential, both for the use of these genotypes in crossing blocks and for cultivation in affected areas.

Salinity affects shoot length, root length, and plant biomass in rice seedlings (KAKAR et al. 2019), being important growth parameters for characterizing tolerance to this stress. Here, the genotypes showed significant variation for the shoot and root traits evaluated in seedlings under salinity (Tables 1 and 2). These results are different, partly, from those observed by DE LEON et al. (2015), that analyzing seedlings of 49 rice genotypes subjected to salinity (12 dS m^{-1}) and found that stress reduced root length, but not significantly. On the other hand, the authors observed that the shoot length was significantly reduced by salinity. Therefore, the shoot would be a better indicator for salinity tolerance in rice seedlings (DE LEON et al. 2015). Seedlings of 33 landraces grown under different levels of salt solution (4, 6, 8, 10, 12 and 14 dS m^{-1}) were evaluated and it was reported that SL, RL and plant biomass are significantly reduced by stress, and the tolerance level varies between genotypes (ALI et al. 2014). Even salinity significantly influencing the three parameters, the authors suggest that SL and plant biomass are better descriptors for tolerance than RL. On the other hand, KAKAR et al. (2019) suggest that root traits are the best descriptors for the characterization for salinity tolerance. This variation in the results between the studies is expected since the trait studied is quantitative, and there are changes in relation to environmental conditions, including the amount of salt and the genetic background used between the studies.

The reduction of the growth parameters under salinity can be explained by the reduction of water uptake by the roots due to osmotic stress, imbalance in the uptake of nutrients due to the accumulation of salts close to the roots, and the accumulation of salts in the tissues, which impacts different metabolic

processes and morpho-physiological traits, including photosynthesis (ALI et al. 2014, KAKAR et al. 2019). Although in this study most genotypes showed a reduction in RP under salinity, and in some genotypes there was an increase in RP in this condition. This increased growth is suggested to be a tolerance mechanism to dealing with stress.

It has already been shown that to avoid Na^+ and Cl^- accumulation in the leaves, salts are excluded from the roots. In addition, the roots also act as barriers, controlling the entry of salts along with the uptake of water. Additionally, they are responsible for the abscisic acid synthesis, one of the main signals during osmotic stress conditions (REDDY et al. 2017). Taking these aspects into account, it is suggested that root is determinant in salinity tolerance. Therefore, in this study, to classify the genotypes in terms of salinity tolerance, in addition to shoot parameters, root parameters were also used (Table 2).

The criterion used in this study to categorize the genotypes into sensitive, moderately sensitive, moderately tolerant and tolerant (Table 2), was efficient mainly to identify contrasting genotypes. In addition, the genotypes previously known as tolerant, such as Bojuru and IAS 12-9 Formosa, remained with this classification in this study. Thus, the genotypes identified as salinity tolerant at the seedling stage can be considered for use in breeding blocks aiming at the development of new varieties. In addition, some cultivars from EPAGRI (Empasc) may be indicated for cultivation in areas with a history of saline stress. However, it should be taken into account that salinity tolerance at the seedling stage is not correlated with salinity tolerance at the vegetative and reproductive stages (KAKAR et al. 2019).

The separation of genotypes by principal component analysis (PCA) (Figure 1) is in agreement with the categorization of genotypes based on the mean RP. As it is a multivariate analysis, PCA allows the simultaneous analysis of multiple parameters, which increases the accuracy of grouping or dispersion of genotypes. This agreement between the analyzes suggests that the mean RP is an efficient method for categorizing genotypes in terms of salinity response.

The dispersion of genotypes in the PCA (Figure 1) allows visualizing the presence of genetic diversity for the studied traits under salinity. Previous reports also demonstrate that, in general, there is genetic diversity for salt-stress tolerance in rice seedlings. A report involving 45 accessions from the International Rice Research Institute (IRRI) and Southern USA showed narrow genetic diversity when using molecular markers, but genotype dispersion was observed when using morphological and physiological characters in response to salinity, indicating the presence of genetic diversity for this trait (DE LEON et al. 2015). In a study with 74 genotypes obtained from IRRI, Philippines, KAKAR et al. (2019) found wide diversity for salinity tolerance, especially when considering root traits. These results demonstrate that it is possible to obtain superior genotypes for salinity tolerance. However, it should be noted here that, in general, domestication and the narrow genetic base of elite parents used in rice breeding programs led to stagnation of genetic gain for several traits of agronomic interest. Therefore, it is essential that accessions available in the germplasm bank (ROY & SHIL 2020), especially non-elite accessions, be introduced in the crossing blocks.

The phenotype of quantitative traits, such as salinity tolerance, is the result of the effect of many genes (genotype), environmental factors and their interactions. Heritability can be used to increase understanding of character inheritance. As mentioned earlier, broad-sense heritability ($H^2 = V_G/V_P$) is the proportion of phenotypic variance conferred by all genetic causes, and narrow-sense heritability ($h^2 = V_A/V_P$) is the proportion of phenotypic variance conferred by additive gene action. The genetic variance, in addition to additive gene action, includes intra-locus (dominance) and inter-locus (epistasis) interactions (WANG et al. 2013). Here, due to the genetic design used, heritability in the broad sense (H^2) was calculated. To facilitate the discussion, in this study, H^2 was classified as low (0–30 %); moderate (30–60 %) and high (>60 %) (ROBINSON et al. 1951).

The heritability of SL was moderate while that of RL was high (Table 1). In a study with rice seedlings under saline stress, using introgression lines, it was also found that the H^2 of SL (0.38) is lower than that of RL (0.98), however at very different values from those found in this study (PURAM et al. 2017). Together, these results demonstrate that SL is more influenced by the environment than RL. Variation in H^2 values of the same trait is common, since heritability is not constant, that is, changes in genetic background and environment lead to changes in heritability values (WRAY & VISSCHER 2008).

The H^2 values for SDW and RDW obtained in this study were considered high (Table 1). Similar values were found in diallel crosses with reciprocals used to estimate the heritability of characters related to salinity tolerance in rice seedlings (MOHAMMADI et al. 2014). The authors found H^2 ranging from 0.60-0.69 and 0.63-0.71 for SDW and RDW, respectively. An H^2 of 0.80 for SDW, very similar to that found in this study has been reported (PURAM et al. 2017). With this, it is suggested that most of the variation observed for dry matter is of a genetic cause, which can facilitate the selection process carried out by breeders.

CONCLUSION

In the studied collection, tolerant and moderately salinity tolerant genotypes were identified at the seedling stage, which may contribute to the development of new tolerant genotypes. Among salinity tolerant genotypes can be highlighted M1150, Lemont, Empasc-101, BRS-Bojuru, Meio-Chumbinho, Empasc-105, Empasc-104, IAS-12-9-Formosa, Empasc-100 and Rexoro. From the PCA analysis, it was possible to verify the occurrence of genetic diversity in the studied traits in seedlings submitted to salinity. Furthermore, the heritability analysis showed that most of the variation observed in the studied traits is of genetic cause, which can facilitate the selection process.

ACKNOWLEDGMENT

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